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☐ 1: AAA03470. cutinase...[gi:416218]

BLink, Domains, Links

LOCUS AAA03470 209 aa linear PLN 16-NOV-1993
 DEFINITION cutinase.
 ACCESSION AAA03470
 VERSION AAA03470.1 GI:416218
 DBSOURCE locus ABU03393 accession U03393.1
 KEYWORDS .
 SOURCE Alternaria brassicicola
 ORGANISM Alternaria brassicicola
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
 REFERENCE 1 (residues 1 to 209)
 AUTHORS Yao,C. and Koeller,W.
 TITLE Cloning and characterization of a cutinase gene from Alternaria
 brassicicola
 JOURNAL Physiol. Mol. Plant Pathol.
 REFERENCE 2 (residues 1 to 209)
 AUTHORS Yao,C.
 TITLE Direct Submission
 JOURNAL Submitted (09-NOV-1993) Chenglin Yao, Plant Pathology, Cornell
 University, Geneva, NY 14456, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..209
 /organism="Alternaria brassicicola"
 /db_xref="taxon:29001"
 Protein 1..209
 /product="cutinase"
 CDS 1..209
 /gene="cutab1"
 /coded_by="join(U03393.1:550..687,U03393.1:744..1235)"
 ORIGIN
 1 mmmnl nllllsk pcqasttrne letgssdacp rtififargs teagnmgalv gpftanales
 61 aygasnvwvq gvvgpytagl venalpagts qaaireaqrl fnlaaskcpn tpitaggysq
 121 gaavmsnaip glsaavqddi kgvvlfgytk nlqnggripn fptskttiyc etgdlvcngt
 181 liitpahllly sdeaavqapt flraqidsa
 //

Revised: August 5, 2002.

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2003-03-11 16:01

NCBI

Sequence revision history

Entrez ?

Revision History for Accession = aaa03470, Version = 1		
<i>gi</i>	<i>Version</i>	<i>Update Date</i>
<u>416218</u>	1	Nov 24 1993 5:18:45:100AM

This sequence was first seen at NCBI on Nov 17 1993 12:06:18:653AM (see Disclaimer)

Result No.	Score	Query		Length	DB	ID	Description
		Match	Length				
1	604	60.5	209	1	CUTI_ALTRB	P41744	alternaria
2	601.5	60.2	228	1	CUTI_MAGGR	P30272	magnaporthe
3	584	58.5	224	1	CUTI_COLGL	PI1373	colletotric
4	564	56.5	223	1	CUTI_ASCRA	P29292	ascochyta r
5	558.5	55.9	228	1	CUTI_COLCA	PI0951	colletotric
6	558	55.9	230	1	CUTI_FUSSC	Q99174	fusarium so
7	553	55.4	230	1	CUTI_FUSSO	P00590	fusarium so
8	550.5	55.1	231	1	CUTI2_FUSSO	Q96ut0	fusarium so
9	548.5	54.9	231	1	CUTI3_FUSSO	Q96us9	fusarium so
10	445	44.5	213	1	CUTI_ASPOR	P52956	aspergillus
11	226	22.6	202	1	CUTI_BTOTCI	Q00298	botrytis ci
12	197.5	19.8	217	1	CUTI1_MYCTU	Q10837	mycobacteri
13	187.5	18.8	219	1	CUTI2_MYCTU	Q50664	mycobacteri
14	167.5	16.8	247	1	CUTI3_MYCTU	Q06318	mycobacteri
15	89	8.9	592	1	XYNB_PSEFL	P23030	pseudomonas
16	88.5	8.9	6486	1	TYCC_BACBR	Q30409	b tyrocidin
17	83	8.3	1293	1	ENFP_ECO57	Q8xbv9	escherichia
18	83	8.3	1356	1	HETI_PODAN	Q00808	podospora a
19	82	8.2	329	1	EBA3_FLAME	P36913	flavobacteri
20	81	8.1	380	1	H181_MYCTE	Q06591	mycobacteri
21	80	8.0	466	1	GSA_SOYBN	P45621	glycine max
22	78.5	7.9	456	1	MURD_ENTFA	Q07108	enterococcu
23	78.5	7.9	481	1	GSA_LYCES	Q40147	lyperosisco
24	78	7.8	377	1	H188_MYCLE	Q9x7b8	mycobacteri
25	78	7.8	743	1	OCTI_HUMAN	PI4859	homo sapien
26	77.5	7.8	525	1	BACA_BACLI	Q68006	b bacitraci
27	76.5	7.7	423	1	Y370_RHIME	Q52997	rhizobium m
28	76.5	7.7	453	1	GATA_CAMJE	Q9pnn2	campylobact
29	76	7.6	363	1	SYRH_BACHD	Q9k9t0	bacillus ha
30	76	7.6	423	1	MYH_SALTY	Q52765	salmonella
31	76	7.6	482	1	YPTI_CABEL	P41879	caenorhabdi
32	75.5	7.6	384	1	RECF_BRUME	Q8yed7	bruceella me
33	75.5	7.6	928	1	PM11_CHLPN	Q86164	chlamydia p

```

Db 13 QASTTRNELETCSSDACPRITIFARGSTGACNMALVGPFTANALESAYGASNVWQGV 72
Qy 59 GGPYDAALATNLPRTGTSQANIDEGKRLFALANOKCPNTPVAGYSGOGAALIAAASEL 118
Db 73 GGPYTAGLVENALPAGTSSQALREARQLENLAACKPPTITAGTSGOGAANVNAIPGL 132
Qy 119 SGAYKEQVKGVALGYTONLQNRGGIPNPRERTKVFQNVGDAVCTGTLITPAHLSTYI 178
Db 133 SAAVODQIKGVVLFQYTKNLQNRGRIPNPTSKTTCYTCTGDLVGNCTLIITPAHLSTYD 192
Qy 179 EARGEAAARFLRDR 192
Db 193 EAAVQAPTEFLRAQI 206

RESULT 2
CUTI_MAGGR
ID CUTI_MAGGR STANDARD; PRT; 228 AA.
AC P30272;
DT 01-APR-1993 (Rel. 25, Created)
RT 01-FEB-1996 (Rel. 33, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
JE Cutinase precursor (EC 3.1.1.74).
GN CUTI
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4091-5-8;
RX MEDLINE=92212279; PubMed=1557023;
RA Sweigard J.A., Chumley F., Valent B.;
RT "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
RT grisea.";
RL Mol. Gen. Genet. 232:174-182(1992).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC permeates the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O -> cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC
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CC
CC EMBL; X61500; CAA43717.1; ALT_TERM.
CC HSSP; P00390; ICDW.
CC InterPro; IPR0000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC KW Hydrolase; Serine esterase; Signal; glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 228
FT DISULFID 49 196
FT DISULFID 127 189
FT ACT_SITE 138 138
FT ACT_SITE 193 193
FT ACT_SITE 206 206
FT CARBOHYD 190 190
SQ SEQUENCE 228 AA; 24276 MW; BR0ACE063B9D4627 CRC64;

Query, Match
Best Local Similarity 60.2%; Score 601.5; DB 1; Length 228;
Matches 117; Conservative 27; Mismatches 50; Indels 1; Gaps 1;

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Qy 1 QUGATENGLESANACPDAILIFARGSTGPGNMGTVPALANGLESIRN-IWIOGVG 59
Db 33 QUNSVNRDLISNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFRNDIWIQGVG 92
Qy 60 GPYDAALATNLPRTGTSQANIDEGKRLFALANOKCPNTPVAGYSGOGAALIAAASEL 119
Db 93 DPYDAALSPNLPAGTTCGATDEAKRMTFLANTKCPNAAVAGGYSGGTAVMNAVSEMP 152
Qy 120 GAYKEQVKGVALGYTONLQNRGGIPNPRERTKVFQNVGDAVCTGTLITPAHLSTYIE 179
Db 153 AAVQDQIKGVVLFQYTKNLQNRGRIPNPTSKTTCYTCTGDLVGNCTLIITPAHLSTY 212
Qy 180 ARGEAARFLRDR 194
Db 213 SSIAAPNWLIRQIRA 227

RESULT 3
CUTI_COLGL
ID CUTI_COLGL STANDARD; PRT; 224 AA.
AC P11373;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN [1]
RP SEQUENCE FROM N.A.
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
RT sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O -> cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC
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CC
CC EMBL; M21443; AAA33042.1; -.
CC PIR; B27451; B27451.
CC HSSP; P00590; ICDW.
CC InterPro; IPR000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC KW Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 16
FT CHAIN 17 224
FT DISULFID 46 194
FT DISULFID 125 187
FT ACT_SITE 136 136

```

```
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 204 204 BY SIMILARITY.
SQ SEQUENCE 224 AA; 23477 MW; 1C5BACEAB469ABFA CRC64;

Query Match
Best Local Similarity 58.5%; Score 584; DB 1; Length 224;
Matches 111; Conservative 28; Mismatches 47; Indels 2; Gaps 1;

QY 7 NGLSSANACPDAILIFARGSTPEGNMGITVGPALANGLES--HIRNIQGVGGPYDA 64
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36 NELETSSSSCPKVIYIFARASTPEGNMGISAGPIVADALERIYGANNVWVGVPYLA 95
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 ALATNLPRTSQANIDEGKELFALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVKE 124
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 DLASNLPDGTSSAAINEARLFTLANTKCPNAAIVSGGYSQGTAVMAGSISGLSTIKN 155
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 125 QVGVVALFGYTONLQNRGGTPNTPRRTKVCNVDGAVCTGTLITPAHLSYTTIARGEA 184
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 QIKGVVLFYTKNLQNLGRIPNFTSKTEVYCDIADAVCVGTILPAHFLYQTDAAVAA 215
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 185 ARELRDRI 192
   |||: ||
Db 216 PRELQARI 223
   |||: ||

RESULT 4
CUTI_ASCRA
ID CUTI_ASCRA STANDARD; PRT; 223 AA.
AC P29292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUT.
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC mitosporic Pezizomycotina; Ascochyta.
OX NCBI_TaxID=5454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 534.65;
RA Tenhaken R., Barz W.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -|- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- INDUCTION: By contact with cutin.
CC -|- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
CC EMBL; X65628; CAA46582.1; -
CC PIR; S21427; S21427.
CC HSP; P00590; ICDW.
CC InterPro; IPR000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 223 CUTINASE.
FT DISULFID 46 192 BY SIMILARITY.
FT DISULFID 124 185 BY SIMILARITY.
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FT ACT_SITE 135 135 BY SIMILARITY.
FT ACT_SITE 189 189 BY SIMILARITY.
FT ACT_SITE 202 202 BY SIMILARITY.
SQ SEQUENCE 223 AA; 23520 MW; 1B82A5ADD1B5E7FB CRC64;

Query Match
Best Local Similarity 56.5%; Score 564; DB 1; Length 223;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IEGLSSANACPDAILIFARGSTPEGNMGITVGPALANGLES--IRNIWQGVGGPYD 63
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 34 IRSELEQSSSCPKAILIFARGSTPEGNMGVSGAVASALEAGADQIWWGVGGPYT 93
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 AALATNLPRTSQANIDEGKELFALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVK 123
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 ADLPSNLPDGTSSAAINEARLFTLANTKCPNAAIVSGGYSQGTAVMAGIAPKLD-AVR 152
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 124 EQVGVVALFGYTONLQNRGGTPNTPRRTKVCNVDGAVCTGTLITPAHLSYTTIARGE 183
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 ARVYGVTLFGYTONQNNKGIDYQEDLQVYCEVGDVLCVDTGLTIITVSHFLYLEAAGP 212
   |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 AARELRDRI 194
   |||: ||
Db 213 APEFLKSKIGA 223
   |||: ||

RESULT 5
CUTI_COLCA
ID CUTI_COLCA STANDARD; PRT; 228 AA.
AC P10951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA.
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5456;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 48574;
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
RT sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -|- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -|- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- INDUCTION: By contact with cutin.
CC -|- PM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -|- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
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CC -----
CC EMBL; M18033; AAA33043.1; -
CC PIR; A27451; A27451.
CC HSP; P00590; ICDW.
CC InterPro; IPR000675; Cutinase.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
```

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DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Signal.
FT CHAIN 1 16 POTENTIAL.
FT CHAIN 17 228 CUTINASE.
FT DISULFID 49 198 BY SIMILARITY.
FT DISULFID 129 191 BY SIMILARITY.
FT ACT_SITE 140 190 BY SIMILARITY.
FT ACT_SITE 195 195 BY SIMILARITY.
FT ACT_SITE 208 208 BY SIMILARITY.
SQ SEQUENCE 228 AA; 23714 MW; 3825D42C23DA139B CRC64;

Query Match 55.9%; Score 558.5; DB 1; Length 228;
Best Local Similarity 57.7%; Pred. No. 1.4e-40;
Matches 109; Conservative 27; Mismatches 50; Indels 3; Gaps 2;

QY 7 NGLSGSANCPDAILIFARGSTPEGNMGITVGPALANGLESH--IRNIWQVGGPYDA 64
DB 39 NELESGSSNCPKVIYIFARASTPEGNMGISAGPIVADALESRYGASQVWVQVGGPYSA 98
Y 65 ALATNF-LPRGTQANIDECKRLFPALANOKCPNTPVVGYSOGAALIAAAYSELGAYK 123
DB 99 DLASNIIPGTSRVAINEAKRLFTLANTRCPNSAVVAGGISQGTAYMASSISELSSTIQ 158
QY 124 EOYKGVALFGYTONLQNRGGIPNYPRTKRVFCNVGDVACTGTLLIIPAHLSYTIARGE 183
DB 159 NQIKGVVLSAITNQLNIGRIPNFSSTKTEVYCALADAVCYGILFILPAHFLYQADAATS 218
QY 184 AARFLDRRI 192
DB 219 APRFLAARI 227

RESULT 6
CUTL_FUSSC
ID CUTL_FUSSC STANDARD; PRT; 230 AA.
AC Q99174;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA.
OS Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=57162;
RN [1]
RP SEQUENCE FROM N.A.
SC STRAIN-PGB 153;
A Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
RA Rees-George J., Rikkerink E.H., Templeton M.D.;
RT "Effect of disruption of a cutinase gene (cutA) on virulence and
RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
RT Cucurbita maxima and C. moschata."
RL Mol. Plant Microbe Interact. 10:355-368(1997).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
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CC -----
DR EMBL; U63335; AAB05922.1;

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DR HSSP; P00590; 2CUT.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PRINTS; PRO0129; CUTINASE.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Signal.
FT SIGNAL 1 16 BY SIMILARITY.
FT CHAIN 17 230 CUTINASE.
FT DISULFID 47 194 BY SIMILARITY.
FT DISULFID 125 187 BY SIMILARITY.
FT ACT_SITE 136 196 BY SIMILARITY.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 204 204 BY SIMILARITY.
SQ SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;

Query Match 55.9%; Score 558; DB 1; Length 230;
Best Local Similarity 55.8%; Pred. No. 1.6e-40;
Matches 110; Conservative 32; Mismatches 51; Indels 4; Gaps 3;

QY 1 QLG-AIENGLESGSANCPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNIWIOG 57
DB 30 QLGTTRDDLLNGNSACADVIFIVARGSTETGNLG-TLGPSIASNLESFCTDGVWIOG 88
QY 58 VGGPYDAALATNFIPLRGTSQANIDECKRLFPALANOKCPNTPVVGYSOGAALIAAAYSE 117
DB 89 VGGAYRATLGDNALPRGTSSAAIREMLGLFQOANTKCPDANTLIAGYSOGAALAAASIED 148
QY 118 LSGAVKQVKGVALFGYTONLQNRGGIPNYPRTKRVFCNVGDVACTGTLLIIPAHLSY 177
DB 149 LDSAIRDKIAGTVLFYTKNLQNRGRIPNYPADRTKVFECNVGDVLTCTGLIIVAPHLAIG 208
QY 178 IEARGEAAFLDRIRA 194
DB 209 PDARGPAPEFLIEKVA 225

RESULT 7
CUTL_FUSSO
ID CUTL_FUSSO STANDARD; PRT; 230 AA.
AC P00590;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase 1 precursor (EC 3.1.1.74).
GN CUTI OR CUTA.
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-T-8;
RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;
RT "Cloning and structure determination of cDNA for cutinase, an enzyme
RT involved in fungal penetration of plants."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89197761; PubMed=2703464;
RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;
RT "Structure of the cutinase gene and detection of promoter activity in
RT the 5'-flanking region by fungal transformation."
RL J. Bacteriol. 171:1942-1951(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=92220194; PubMed=1560844;
RA Martinez C., de Geus P., Lauwereys M., Matthysens G., Cambillau C.;
RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
RT serine accessible to solvent."
RL Nature 356:615-618(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

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